

Genotype version 5.1.4.P5_4578
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MM nucleotide - nucleotide search, using SW model

Run on: March 20, 2003, 09:09:41 : Search time 78 seconds
(without alignments)
159,198 Million cell of data/sec

Hit(s): US-09-530-935-1

Percent score: 14

Sequence: 14

Search table(s): IDENTITY_NMP
Gapop: 10.0 / Gapext: 1.0

Searchset: 588426 seqs, 387737921 residues

Total number of hits satisfying chosen parameters: 1077652

Minimum seq length: 0

Maximum seq length: 200000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Database: 1

Published Affiliations: NA
1: 100% (100%)
2: 100% (100%)
3: 100% (100%)
4: 100% (100%)
5: 100% (100%)
6: 100% (100%)
7: 100% (100%)
8: 100% (100%)
9: 100% (100%)
10: 100% (100%)
11: 100% (100%)
12: 100% (100%)
13: 100% (100%)
14: 100% (100%)

Note: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length (bp)	Description
1	42.9	15	10	Sequence 456, Ap
2	42.9	15	10	Sequence 456, Ap
3	42.9	17	9	Sequence 419, Ap
4	42.9	17	9	Sequence 1310, Ap
5	42.9	17	9	Sequence 1311, Ap
6	42.9	17	9	Sequence 1312, Ap
7	42.9	17	9	Sequence 1313, Ap
8	42.9	17	9	Sequence 1314, Ap
9	42.9	17	9	Sequence 1315, Ap
10	42.9	17	9	Sequence 1316, Ap
11	42.9	17	9	Sequence 1317, Ap
12	42.9	17	9	Sequence 1318, Ap
13	42.9	17	9	Sequence 1319, Ap
14	42.9	17	9	Sequence 1320, Ap
15	42.9	17	9	Sequence 1321, Ap
16	42.9	17	9	Sequence 1322, Ap
17	42.9	17	9	Sequence 1323, Ap
18	42.9	17	9	Sequence 1324, Ap
19	42.9	17	9	Sequence 1325, Ap
20	42.9	17	9	Sequence 1326, Ap

ALIGNMENTS

20	42.9	17	10	US-09-866-108-575	Sequence 456, Ap
21	42.9	17	10	US-09-866-108-576	Sequence 456, Ap
22	42.9	17	10	US-09-866-108-577	Sequence 456, Ap
23	42.9	17	10	US-09-866-108-578	Sequence 456, Ap
24	42.9	17	10	US-09-866-108-579	Sequence 456, Ap
25	42.9	17	10	US-09-866-108-580	Sequence 456, Ap
26	42.9	17	10	US-09-866-108-581	Sequence 456, Ap
27	42.9	17	10	US-09-866-108-582	Sequence 456, Ap
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31	42.9	17	10	US-09-866-108-586	Sequence 456, Ap
32	42.9	17	10	US-09-866-108-587	Sequence 456, Ap
33	42.9	17	10	US-09-866-108-588	Sequence 456, Ap
34	42.9	17	10	US-09-866-108-589	Sequence 456, Ap
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42	42.9	17	10	US-09-866-108-597	Sequence 456, Ap
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44	42.9	17	10	US-09-866-108-599	Sequence 456, Ap
45	42.9	17	10	US-09-866-108-600	Sequence 456, Ap

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US-09-866-108-597
US-09-866-108-598
US-09-866-108-599
US-09-866-108-600

Query Match: 42.963 Score: 63 DB: 10; Length: 15
Post local similarity: 42.963 Pval: No. 2,000,000
Matches: 63 Conserved: 63 Mismatches: 83 Indels: 03 Gaps: 03

DB: 15 1159 Alignment: 2

1

2

[illegible][illegible]


```

RESULT 1:
US-09-071-845-1829/6
Sequence: 1829, Application US/09071845
Patent No.: 6142967
GENERAL INFORMATION:
APPLICANT: Susan O'Hlum
APPLICANT: Dan L. Sullivan
APPLICANT: James Mesrobian
APPLICANT: Sean Sullivan
TITLE OF INVENTION: REPAIR OF TREATMENT OF
TITLE OF INVENTION: DISAPPEARANCE OF SCALDS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
NUMBER OF INVENTION: 6429001 (1 (AM-1))
NUMBER OF SEQUENCES: 2390
ADDRESS/INVENTOR ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
MODIFIER READABLE FORM:
MODIFIER TYPE: 3.5" Diskette, 1.44 MB
MODIFIER TYPE: Storage
COMPUTER: IBM Compatible
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/071,845
FILING DATE:
CLASSIFICATION:
FOR APPLICATION DATA:
APPLICATION NUMBER: 07/071,845
FILING DATE: August 17, 1994
APPLICATION NUMBER: 07/071,845
FILING DATE: January 19, 1994
APPLICATION NUMBER: 07/071,845
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/071,845
FILING DATE: December 7, 1992
NAME: Withing, Richard J.
REGISTRATION NUMBER: 42,827
REFERENCE TO: 42,827
FIELD OF INVENTION: INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELEPHONE: 67-4510
TELEPHONE: 67-4510
INFORMATION FOR SEQ ID NO: 1829:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
Topology: linear
US-09-071-845-1829
Query Match: 42.9% Score 6 DB 3 Length 17
Best Local Similarity: 42.9% Pred. No. 1 3e-04
Matches: 6 Conserved 0 Mismatches: 8 Indels: 0 Gaps: 0
14 HIGGALGATGTCG 1

```

```

APPLICANT: Susan O'Hlum
APPLICANT: Dan L. Sullivan
APPLICANT: James Mesrobian
APPLICANT: Sean Sullivan
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TITLE OF INVENTION: DISAPPEARANCE OF SCALDS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
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STREET: Suite 4700
CITY: Los Angeles
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ZIP: 90071-2066
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MODIFIER TYPE: 3.5" Diskette, 1.44 MB
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FILING DATE: December 7, 1992
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NAME: Withing, Richard J.
REGISTRATION NUMBER: 42,827
REFERENCE TO: 42,827
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TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELEPHONE: 67-4510
TELEPHONE: 67-4510
INFORMATION FOR SEQ ID NO: 1829:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
Topology: linear
US-09-071-845-1829
Query Match: 42.9% Score 6 DB 3 Length 17
Best Local Similarity: 42.9% Pred. No. 1 3e-04
Matches: 6 Conserved 0 Mismatches: 8 Indels: 0 Gaps: 0
14 HIGGALGATGTCG 1
Search completed: March 20, 2003, 06:19:13
Job Time: 61 seconds

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 GetDoc version 5.1.4_15_4576

Molecular Sieves, using SW model

March 20, 2004, 05:21:44 ; Speech time 1665.500000
(Gibson & Ingham's)

[illegible]
$$\lim_{n \rightarrow \infty} \int_0^{\infty} e^{-\lambda t} f(t) dt = E[f(X)] = \sum_{j=0}^{\infty} p_j f(j)$$

1. The first part of the paper is devoted to the study of the asymptotic behavior of the solutions of the system (1) as $\epsilon \rightarrow 0$. It is shown that the solutions of the system (1) converge to the solutions of the system (2) in the sense of the weak convergence in the space $L^2(\Omega; \mathbb{R}^n)$.

IDENTITY_100: 100% identical

Search: 2054640 seqs, 1451402878 residues

Total number of hits satisfying chosen parameters: 410/9280

[illegible]

Los Angeles Mitchell

Listed first 45 summaries

1. *Introduction*
 2. *Background*
 3. *Methodology*
 4. *Results*
 5. *Discussion*
 6. *Conclusion*
 7. *References*
 8. *Appendix*
 9. *Index*
 10. *Table of Contents*

1:	ab:ba:	*
2:	ab:baq:	*
3:	ab:ba:	*
4:	ab:ba:	*
5:	ab:ba:	*
6:	ab:ba:	*
7:	ab:ba:	*
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39:	ab:ba:	*
40:	ab:ba:	*
41:	ab:ba:	*

From N_0 is the number of results predicted by chance to have a

Score greater than or equal to the score of the result, both filtered and is derived by analysis of the total score distribution.

SIMPLANK 11.5

Result No.	Score	Yearly		ID	Description
		Match	Location		
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C 2	6	42.9	15	6	AK056571 Superfence
C 3	6	42.9	15	6	AK056738 Superfence
C 4	6	42.9	15	6	AK114390 Superfence
C 5	6	42.9	15	6	AK114711 Superfence
C 6	6	42.9	15	6	AK100916 Superfence
C 7	6	42.9	15	6	AK055895 M262 Superfence
C 8	6	42.9	15	6	E35652 Infection of E35697 Infection of E35697 Superfence
C 9	6	42.9	15	6	AK142923 Superfence
C 10	6	42.9	15	6	AK142923 Superfence
C 11	6	42.9	17	6	AK05414 Superfence
C 12	6	42.9	17	6	AK09621 Superfence
C 13	6	42.9	17	6	AK044419 Superfence
C 14	6	42.9	17	6	AK057460 Superfence
C 15	6	42.9	17	6	AK057625 Superfence
C 16	6	42.9	17	6	AK057702 Superfence
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C 40	6	42.9	17	6	AK115460 Superfence
C 41	6	42.9	17	6	AK115460 Superfence
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C 43	6	42.9	18	6	AK095484 Superfence
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ALIGNMENT

[illegible]

FEATURES: Vienna International Institute for Biotechnology, et al. (10)

SOURCE:

1. 15
/organism "synthetic construct"

misc_journals

1. 15
/note "Molecular Biology"

BASE COUNT: 5 a 6 c 2 g 2 t

ORIGIN:

Query Match: 42.9% Score 62 DB 62 Length 153
Best Local Similarity: 42.9% Pred. No. 1.20e06
Matches: 62 Conserved 62 Mismatches 82 Indels 02 Gaps 02

QY: 1 TTTGNNNNNNNNNN 14
DB: 14 TTTGNNNNNNNNNN 1

RESULT: 7

BASE COUNT: 15 bp DNA Linear PAI 1a JUN-2001

ORIGIN: Novel probes for the detection of Mycobacterium

REFERENCE: 1 (bases 1 to 15)
Stender, H., Lund, K., and Møllerup, T. A.

ORIGIN: Novel probes for the detection of Mycobacterium

REFERENCE: 1 (bases 1 to 15)
Stender, H., Lund, K., and Møllerup, T. A.

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REFERENCE: 1 (bases 1 to 15)
Stender, H., Lund, K., and Møllerup, T. A.

ORIGIN: Novel probes for the detection of Mycobacterium

REFERENCE: 1 (bases 1 to 15)
Stender, H., Lund, K., and Møllerup, T. A.

ORIGIN: unclassified

REFERENCE: 1 (bases 1 to 15)
Stender, H., Lund, K., and Møllerup, T. A.

ORIGIN: Novel probes for the detection of Mycobacterium

BASE COUNT: 7 a 4 c 2 g 2 t

ORIGIN:

Query Match: 42.9% Score 62 DB 62 Length 153
Best Local Similarity: 42.9% Pred. No. 1.20e06
Matches: 62 Conserved 62 Mismatches 82 Indels 02 Gaps 02

QY: 1 TTTGNNNNNNNNNN 14
DB: 14 TTTGNNNNNNNNNN 1

RESULT: 9

BASE COUNT: 2 t

ORIGIN: Novel probes for the detection of Mycobacterium

REFERENCE: 1 (bases 1 to 15)
Stender, H., Lund, K., and Møllerup, T. A.

ORIGIN: Novel probes for the detection of Mycobacterium

REFERENCE: 1 (bases 1 to 15)
Stender, H., Lund, K., and Møllerup, T. A.

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Stender, H., Lund, K., and Møllerup, T. A.

1
2
3

4

The panel for nucleic acid molecules having a hammer head motif is used for the treatment of arthritis, including, but not limited to, rheumatoid arthritis of autoimmune diseases.

Example 1 (see Fig. 3a) (Fig. 3a) (Fig. 3a)

The present invention describes a novel sequence for nucleic acid (NA) having a hammer head motif (HM) complementary (C) at least 5' flanking a hammer head motif (HM) modification at position 4 of the RNA (111) at least 2' flanking modification and (iv) a 4'-end modification. The RNA's can inhibit cell growth and stimulate production in the cell. It is a modification of the RNA's for the treatment of arthritis, particularly osteoarthritis or rheumatoid arthritis. The RNA's can also be used to treat and/or prevent cells of a bone to induce calcification. The present invention of a short, they can also be used for enhancing start tolerance of the treated arthritis disease, and for treating arthritis and other inflammatory conditions. The RNA's can also be used in diagnosis, therapeutic therapy, impacts on the expression of a cell cycle without affecting the cell cycle of cells, and/or expression which accompany treatment with retinoids and decarboxylase. The expression of the sequence required to arrest a then gene for treatment. The expression of arthritis, osteoarthritis, and as binding specific, the present sequence is used in the exemplification of the present invention.

Example 1 (see Fig. 3a) (Fig. 3a) (Fig. 3a)

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The panel for nucleic acid molecules having a hammer head motif is used for the treatment of arthritis, including, but not limited to, rheumatoid arthritis of autoimmune diseases.

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Example 1 (see Fig. 3a) (Fig. 3a) (Fig. 3a)

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17. Similar: The present sequence represents a primer used in the
 18. amplification of the present invention.

19. Sequence: 15 BP, 7 A, 4 C, 2 G, 2 T, 0 other.

20. Query Match: 42.98% Score 62 BP 20; Length 15;

21. Best Local Similarity: 42.98% (Prod. No. 1,16,05)

22. Matches: 6, Conservative: 0, Mismatches: 8, Indels: 0, Gaps: 0

23. 1 HHHHHHHHHHHH 14

24. 14 HHHHHHHHHHHH 1

25. 14 HHHHHHHHHHHH 1

26. 14 HHHHHHHHHHHH 1

27. 14 HHHHHHHHHHHH 1

28. 14 HHHHHHHHHHHH 1

29. 14 HHHHHHHHHHHH 1

30. 14 HHHHHHHHHHHH 1

31. 14 HHHHHHHHHHHH 1

32. 14 HHHHHHHHHHHH 1

33. 14 HHHHHHHHHHHH 1

34. 14 HHHHHHHHHHHH 1

35. 14 HHHHHHHHHHHH 1

36. 14 HHHHHHHHHHHH 1

37. 14 HHHHHHHHHHHH 1

38. 14 HHHHHHHHHHHH 1

39. 14 HHHHHHHHHHHH 1

40. 14 HHHHHHHHHHHH 1

41. 14 HHHHHHHHHHHH 1

42. 14 HHHHHHHHHHHH 1

43. 14 HHHHHHHHHHHH 1

44. 14 HHHHHHHHHHHH 1

45. 14 HHHHHHHHHHHH 1

46. 14 HHHHHHHHHHHH 1

47. 14 HHHHHHHHHHHH 1

48. 14 HHHHHHHHHHHH 1

49. 14 HHHHHHHHHHHH 1

50. 14 HHHHHHHHHHHH 1

51. 14 HHHHHHHHHHHH 1

52. 14 HHHHHHHHHHHH 1

53. 14 HHHHHHHHHHHH 1

54. 14 HHHHHHHHHHHH 1

55. 14 HHHHHHHHHHHH 1

56. 14 HHHHHHHHHHHH 1

57. 14 HHHHHHHHHHHH 1

58. 14 HHHHHHHHHHHH 1

59. 14 HHHHHHHHHHHH 1

60. 14 HHHHHHHHHHHH 1

61. 14 HHHHHHHHHHHH 1

62. 14 HHHHHHHHHHHH 1

63. 14 HHHHHHHHHHHH 1

64. 14 HHHHHHHHHHHH 1

65. 14 HHHHHHHHHHHH 1

66. 14 HHHHHHHHHHHH 1

67. 14 HHHHHHHHHHHH 1

68. 14 HHHHHHHHHHHH 1

69. 14 HHHHHHHHHHHH 1

80. Sequence: 15 BP, 1 A, 1 C, 2 G, 1 T, 0 other.

81. Query Match: 42.98% Score 62 BP 21; Length 15;

82. Best Local Similarity: 42.98% (Prod. No. 1,16,05)

83. Matches: 14, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

84. 1 HHHHHHHHHHHH 14

85. 14 HHHHHHHHHHHH 1

86. 14 HHHHHHHHHHHH 1

87. 14 HHHHHHHHHHHH 1

88. 14 HHHHHHHHHHHH 1

89. 14 HHHHHHHHHHHH 1

90. 14 HHHHHHHHHHHH 1

91. 14 HHHHHHHHHHHH 1

92. 14 HHHHHHHHHHHH 1

93. 14 HHHHHHHHHHHH 1

94. 14 HHHHHHHHHHHH 1

95. 14 HHHHHHHHHHHH 1

96. 14 HHHHHHHHHHHH 1

97. 14 HHHHHHHHHHHH 1

98. 14 HHHHHHHHHHHH 1

99. 14 HHHHHHHHHHHH 1

100. 14 HHHHHHHHHHHH 1

101. 14 HHHHHHHHHHHH 1

102. 14 HHHHHHHHHHHH 1

103. 14 HHHHHHHHHHHH 1

104. 14 HHHHHHHHHHHH 1

105. 14 HHHHHHHHHHHH 1

106. 14 HHHHHHHHHHHH 1

107. 14 HHHHHHHHHHHH 1

108. 14 HHHHHHHHHHHH 1

109. 14 HHHHHHHHHHHH 1

110. 14 HHHHHHHHHHHH 1

111. 14 HHHHHHHHHHHH 1

112. 14 HHHHHHHHHHHH 1

113. 14 HHHHHHHHHHHH 1

114. 14 HHHHHHHHHHHH 1

115. 14 HHHHHHHHHHHH 1

116. 14 HHHHHHHHHHHH 1

117. 14 HHHHHHHHHHHH 1

118. 14 HHHHHHHHHHHH 1

119. 14 HHHHHHHHHHHH 1

120. 14 HHHHHHHHHHHH 1

121. 14 HHHHHHHHHHHH 1

122. 14 HHHHHHHHHHHH 1

123. 14 HHHHHHHHHHHH 1

124. 14 HHHHHHHHHHHH 1

125. 14 HHHHHHHHHHHH 1

126. 14 HHHHHHHHHHHH 1

127. 14 HHHHHHHHHHHH 1

128. 14 HHHHHHHHHHHH 1

129. 14 HHHHHHHHHHHH 1

130. 14 HHHHHHHHHHHH 1

131. 14 HHHHHHHHHHHH 1

132. 14 HHHHHHHHHHHH 1

80. Sequence: 15 BP, 1 A, 1 C, 2 G, 1 T, 0 other.

81. Query Match: 42.98% Score 62 BP 21; Length 15;

82. Best Local Similarity: 42.98% (Prod. No. 1,16,05)

83. Matches: 14, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

84. 1 HHHHHHHHHHHH 14

85. 14 HHHHHHHHHHHH 1

86. 14 HHHHHHHHHHHH 1

87. 14 HHHHHHHHHHHH 1

88. 14 HHHHHHHHHHHH 1

89. 14 HHHHHHHHHHHH 1

90. 14 HHHHHHHHHHHH 1

91. 14 HHHHHHHHHHHH 1

92. 14 HHHHHHHHHHHH 1

93. 14 HHHHHHHHHHHH 1

94. 14 HHHHHHHHHHHH 1

95. 14 HHHHHHHHHHHH 1

96. 14 HHHHHHHHHHHH 1

97. 14 HHHHHHHHHHHH 1

98. 14 HHHHHHHHHHHH 1

99. 14 HHHHHHHHHHHH 1

100. 14 HHHHHHHHHHHH 1

101. 14 HHHHHHHHHHHH 1

102. 14 HHHHHHHHHHHH 1

103. 14 HHHHHHHHHHHH 1

104. 14 HHHHHHHHHHHH 1

105. 14 HHHHHHHHHHHH 1

106. 14 HHHHHHHHHHHH 1

107. 14 HHHHHHHHHHHH 1

108. 14 HHHHHHHHHHHH 1

109. 14 HHHHHHHHHHHH 1

110. 14 HHHHHHHHHHHH 1

111. 14 HHHHHHHHHHHH 1

112. 14 HHHHHHHHHHHH 1

113. 14 HHHHHHHHHHHH 1

114. 14 HHHHHHHHHHHH 1

115. 14 HHHHHHHHHHHH 1

116. 14 HHHHHHHHHHHH 1

117. 14 HHHHHHHHHHHH 1

118. 14 HHHHHHHHHHHH 1

119. 14 HHHHHHHHHHHH 1

120. 14 HHHHHHHHHHHH 1

121. 14 HHHHHHHHHHHH 1

122. 14 HHHHHHHHHHHH 1

123. 14 HHHHHHHHHHHH 1

124. 14 HHHHHHHHHHHH 1

125. 14 HHHHHHHHHHHH 1

126. 14 HHHHHHHHHHHH 1

127. 14 HHHHHHHHHHHH 1

128. 14 HHHHHHHHHHHH 1

129. 14 HHHHHHHHHHHH 1

130. 14 HHHHHHHHHHHH 1

131. 14 HHHHHHHHHHHH 1

132. 14 HHHHHHHHHHHH 1

